



Clarice R. Weinberg, Ph.D.

Chief, Biostatistics Branch

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Education:

Simmons College, Boston, MA	1972 BS Mathematics
Brandeis University, Waltham, MA	1974 M.A. Mathematics
University of Washington, Seattle, WA	1980 Ph.D. Biomathematics

Epidemiology is our best tool for studying human health effects of environmental exposures; unfortunately, this tool is inherently imperfect and prone to imprecision and biases. A general research theme of mine has been the development of improved methods for design and analysis that account for sources of bias, missing data, response heterogeneity, and mismeasurement in epidemiologic studies. Methodologic research is most fruitful when it arises in the context of real applications to epidemiology, and my extensive collaborations with epidemiologists at NIEHS have inspired nearly all of this work.

I am also interested in developing improved designs and methods of analysis to elucidate the joint etiologic roles of genetic and environmental susceptibility factors. Complex diseases, such as birth defects, heart diseases, neuro-degenerative disease, and cancer, are caused by time and the combined action of genetic susceptibility factors and exposures. One understudied area is the relation between the prenatal environment and health. Of particular interest is the interplay between genetic factors (both maternal and fetal) and maternal exposures in influencing fetal survival, embryologic development and postnatal longterm health. Methods being developed in this area will be applied to data from the ongoing study of oral clefting (cleft lip and palate) being

carried out in Norway (with Allen Wilcox as the Senior Investigator for NIEHS), and to a larger collaborative analysis involving data from Denmark, Norway, Iowa, and the Phillipines.

I am also currently collaborating with Dr. Dale Sandler of the Epidemiology Branch in initiating a major cohort study of breast cancer, called the Sister Study. We plan to recruit 50,000 women who are each the sister of a woman with breast cancer. Because they are sisters of women with cancer, the cohort will be enriched for the presence of susceptibility genes, and this enrichment will markedly enhance our statistical power for detecting gene-by-environment interactions, compared to a similarly-sized random cohort of women. We are currently just beginning our Phase I recruitment.

Selected Recent Presentations:

2001-June-14, Epidemiology Congress, Methods Plenary.

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Selected Recent Publications:

Curtis, K.M, Savitz, D.A., Weinberg, C.R. and Arbuckle, T.E. The effect of pesticide exposure on time to pregnancy. *Epidemiology* 10(2): 112-117, 1999.

Dunson, D. Perrault, S., Chapin, R., and Weinberg, C.R. Summarizing the motion of self-propelled cells: applications to sperm motility. *Biometrics* 55:537-543, 1999.

Weinberg, C.R. and Umbach, D.M. Using pooled exposure assessment to improve efficiency in case-control studies. *Biometrics* 55(3): 718-726, 1999.

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Wilcox, A.J., Baird, D.D. and Weinberg, C.R. Time of implantation of the conceptus and loss of pregnancy. *New England Journal of Medicine* 340(23): 1796-9, 1999.

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Janowsky, E.C., Lester, G.E., Weinberg, C.R., Millikan, R.C., Schildkraut, J. M., Garrett, P.A., Hulka, B.S. The association between low levels of 1,25-dihydroxy vitamin D and breast cancer risk. *Public Health Nutrition* 2(3): 283-91, 1999.

Dunson, D., Baird, D.D., Wilcox, A.J. and Weinberg, C.R. Day-specific probabilities of clinical pregnancy based on two studies with imperfect measures of ovulation. *Human Reproduction* 14(7): 1835-9, 1999.

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Dunson, D. and Weinberg, C.R. Modeling human fertility in the presence of measurement error. *Biometrics* 56:288-92, 2000.

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Dunson, D.B., Weinberg, C.R., Baird, D.D., Kesner, J., and Wilcox, A.J. Assessing human fertility using several markers of ovulation. *Statistics in Medicine*, 20(6): 965-78, 2001.

Dunson, D.B. Weinberg, C.R. and Wilcox, A.J. Modeling multiple ovulation, fertilization, and embryo survival in human fertility studies. *Biostatistics* 2(2): 131-146, 2001.

Rieger, R., Kaplan, N. and Weinberg, C.R. Efficient use of sibling data for testing for linkage and association. *Genetic Epidemiology*, 20(2): 175-91, 2001.

Li, L., Darden, T.A., Weinberg, C.R., Levine, A.J. and Pedersen, L.G. Gene assessment and sample classification for gene expression data using a genetic algorithm/k-nearest neighbor method. *Combinatorial Chemistry and High Throughput Screening* 4(8): 727-39, 2001.

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Hoffman, Elaine Borland, Sen, P.K., and Weinberg, C.R. Within-cluster resampling. *Biometrika* 88(4):1121-34, 2001.

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Association 286(14): 1759-61, 2001.

Rieger, R. and Weinberg, C.R. Analysis of clustered binary outcomes using within-cluster paired resampling. *Biometrics* 58:332-341, 2002.

Infante-Rivard, C., Rivard, G-E, Yotov, W., Genin, E., Guiguet, M., Weinberg, C., Gauthier R., Feoli-Fonseca, J-C Absence of association of thrombophilic polymorphisms with intrauterine growth restriction. *New England Journal of Medicine*: 347(1): 19-25, 2002.

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Peddada, S.D., Lobenhofer, E.K., Li, L., Afshari, C.A., Weinberg, C.R., Umbach, D.M. Gene selection and clustering for time-course and dose-response microarray experiments using order-restricted inference. *Bioinformatics* 19(7):834-41, 2003.

Weinberg, C.R. and Morris, R. Invited Commentary: Testing for Hardy-Weinberg disequilibrium using a genome SNP scan based on cases only. *American Journal of Epidemiology* 158(5):401-3, 2003.

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Liu, D., Weinberg, C.R. and Peddada, S.D. Association and coherence of the activation times of cell-cycling genes under different experimental conditions: A geometric approach, in press, *Bioinformatics*, 2004.

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SAS code to fit log-linear models for offspring genotype effects, maternal genotype effects, and imprinting. Included is an output file that you can check output from your computer against. Developed by Richard Morris and Clare Weinberg.

[Log_Linear_Model.lst](#) Sample output (updated 2004/02/05)

[Log_Linear_Model.sas](#) SAS code (updated 2004/02/05)

SAS code to fit polytomous and additive logistic models for offspring genotype effects. These models are described in the paper "A Method Using Complete and Incomplete Trios to Identify Genes Related to a Quantitative Trait", by Emily Kistner and Clare Weinberg, which is in press in *Genetic Epidemiology*.

[AdditiveSASrev.doc](#) is the Additive Logistic Model

[ADDQPLEMSAS.doc](#) is the Additive Logistic Model for Missing Parents

[QPLEMSAS.doc](#) is the Polytomous Logistic Model

[completeQPLSAS.doc](#) is the Polytomous Logistic Model for Missing Parents

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